Claim 1 stands rejected as anticipated by US Patent No. 6,303,303 of Green. In order to support an anticipation rejection, the Examiner must point to each and every element of the claimed invention in the single reference. Neither the prior nor the current Examiner have met this standard. Thus, the rejection should be withdrawn as was the rejection over US Patent No. US 5,853,979 which contains an identical disclosure (being the patent of which the '303 patent is a divisional).

In the Green patents, the standard data trace is one which should (absent mutation or error) be the same as the experimental fragment. The analysis of the two traces is done to determine the stretching and shifting which is needed to make the experimental trace look like the standard. Thus, in Green, a polynomial function is determined to define the stretching and shifting which is needed to make the experimental trace look like the standard trace. In the Green patents, there is no analysis of the standard data trace to find the times at which peaks actually occur and thus the times at which peaks should occur in an experimental data trace run under the same conditions. There is also no use of a defined time scale to sample for peaks.

The Examiner has again oversimplified and mischaracterized the matter by stating that all that is required in the present claims is that "experimental data be compared to a reference trace taken at a time location." This statement is incorrect in several respects. First of all, in the present invention, there is no **comparison** between the reference trace and the experimental data trace as that term is used in Green. There is only the identification of a list of times that correspond to peak locations from the reference trace and the use of these times to direct sampling of the experimental trace. Second, the isolated steps of Green that happen to use similar words like "time," do not equal that which is claimed.

For example, step (b) of claim 1 reads:

> (b) evaluating the reference DNA sequencing data traces to determine a corrected time scale **indicative of migration times at which peaks should occur.**

The Examiner has not pointed to where in the Green patent this step is performed, and cannot do so because no such step is performed. Green does not identify the locations of peaks in the

reference data trace and does not determine a corrected time scale based on the positions of peaks in the reference data trace. Indeed, notwithstanding the Examiner's statement (without citation) that Green teaches "normalization of spacing between peaks using a second order polynomial to give a corrected time scale," the words "corrected" and "time scale" appear nowhere in the Green Patents. This is not surprising since Green has nothing to do with correction of time scale, but rather with using the second order or higher polynomial to make two fragments look alike (regardless of the time scale). Furthermore, this process is performed as a modification to the experimental data trace. The present invention does not rely on changing the experimental data trace, but instead uses the reference data trace to establish specific windows in time in which to look for peaks.

Finally, the Examiner incorrectly asserts that "all that is disclosed includes 'sampling the experimental data trace(s) at time points.'" Claim 1, however says more than this. Step (c) "sampling the experimental DNA sequencing data trace(s) at time points **determined by the corrected time scale**" which is the corrected time scale determined in step (b) that says where the peaks ought to be.

For the foregoing reasons, Applicants submit that the Examiner has failed to present a sound rejection under 35 USC § 102 with respect to claim 1 and the claims dependent thereon. Thus this rejection should be withdrawn. Applicants further point out that the Examiner has not even attempted to point out where in the reference the specific limitations of the dependent claims are found. For example, claim 2 reads:

> 2. The method of claim 1, wherein the step of evaluating the reference DNA sequence data traces includes the steps of:
>
> (i) identifying a plurality of peaks in the reference DNA sequencing data traces, and creating a data table containing the number of each peak based on the known sequence of the polynucleotide, and the position of each peak in the reference DNA sequencing data trace;
>
> (ii) identifying a set of coefficients for a polynomial effective to substantially linearize a plot of peak number versus separation between adjacent peaks; and

(iii) creating from the coefficients and the polynomial a corrected time scale which reflects the positions at which a peak should occur at any given point in a sequencing data trace.

Green does not disclose making or linearizing a plot of peak number versus peak separation for the reference trace. How then could this claim be anticipated? Where in Green is there a disclosure of selecting "a defined number of bands are selected for evaluation from each of the reference DNA sequencing data traces" as recited in claim 6? The Examiner has not said. The rejection is similarly defective with respect to other dependent claims that are erroneously lumped under the single anticipation rejection.

Claim 11 and the claims dependent thereon are method claim directed to a method for determining the sequence of a target polynucleotide. Claim 11 contains substantially the same limitations as claim 1, and therefore is not anticipated for the same reasons. Further, the Examiner has not specifically identified how the dependent claims in this claim set can be deemed to be anticipated.

Claims 21 and 22 are apparatus claims. It clearly states that it includes "a processor, operatively programmed to evaluate the reference DNA sequencing traces to determine a corrected time scale at which points should occur." Green does not disclose a process in which this step is performed, and thus manifestly does not teach an apparatus programmed to perform this step. Furthermore, claims 21 requires "a processor, operatively programmed to sample the experimental DNA sequencing traces at time points determined by the corrected time scale. " Green determines no corrected time scale and does not teach sampling of an experimental DNA trace at selected times based on such a scale. Thus, Green plainly does not teach an apparatus programmed to perform this step. Thus, Green does not anticipate the apparatus claims 21 and 22.

Finally, the Examiner has rejected claims 21 and 22 for obviousness-type double patenting over claims 1-14 of Green. Again, the Examiner has not actually compared the limitations of the claims, but has made a general statement, namely that "the apparatus of Green

can perform all of the limitations set forth in the instant application" without explanation of how this could be the case. The data processing portion of claim 1 of Green reads as follows:

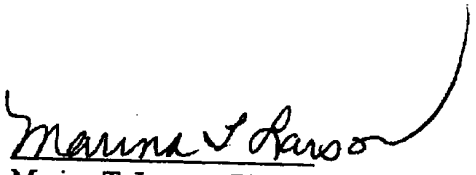
> (d) means for causing the computer processor to determine one or more normalization coefficients for the experimental fragment pattern, said normalization coefficients being selected to provide a high degree of overlap between a normalized fragment pattern obtained by applying the normalization coefficients to the experimental fragment pattern and the standard fragment pattern.

This limitation calls for processing in which coefficients are found to make an experimental fragment pattern look like a standard fragment pattern. In contrast, claim 21 requires that the processor be programmed to perform very different functions: namely (1) "to evaluate the reference DNA sequencing data traces to determine a corrected time scale indicative of migration times at which peaks should occur;" (2) "to sample the experimental DNA sequencing data traces at time points determined by the corrected time scale" and (3) to assign a base number to each peak found in the experimental DNA sequencing data traces based upon the corrected time scale, thereby obtaining information about the sequence of the target polynucleotide. The Examiner has not said how a processor programmed to identify a polynomial that will make two data traces look alike can be assumed to be able to determine a corrected time scale for one trace alone, or to direct the sample of the other trace at the identified time points. This being the case, the Examiner has not set forth a sufficient basis for the rejection for obviousness-type double patenting.

VGEN.P-056
PATENT APPLICATION

In view of the foregoing, Applicants submit that this application is in form for allowance. A Notice of Appeal is being filed concurrently by mail to afford the Examiner time to review this application.

Respectfully submitted,



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